

SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Duft, Bradford
 Kolterman, Orville
- (ii) TITLE OF THE INVENTION: METHODS FOR TREATING OBESITY
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LYON & LYON
 - (B) STREET: 633 WEST FIFTH STREET, SUITE 4700
 - (C) CITY: LOS ANGÈLES
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/870,762
 - (B) FILING DATE: 06-JUN-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: DUFT, BRADFORD J
 - (B) REGISTRATION NUMBER: 32,219
 - (C) REFERENCE/DOCKET NUMBER: 226/104
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-552-8400
 - (B) TELEFAX: 619-552-0159
 - (C) TELEX:

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- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: \ amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE \TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: $\setminus 2, 7$
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

1 5 10 15

Leu Val His Ser Ser Asn Asn Phe Cly Pro Ile Leu Pro Pro Thr
20 25 30

Asn Val Gly Ser Asn Thr Tyr

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe 10 Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr 25 Asn Val Gly Ser\Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3\7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: 1\inear
- (ii) MOLECULE TYPE \ Peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION, amidated Tyr
- (xi) SEQUENCE DESCRIPTION:\SEQ ID NO:3:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe 5 15 Leu Val Arg Ser Ser Asn Asn Phe Gly Rro Ile Leu Pro Ser Thr 20 Asn Val Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7

- (D)\OTHER INFORMATION: disulfide bridge between the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe 10 Leu Val His Ser Ser\ Asn Asn Phe Gly Ala Ile Leu Pro Ser Thr 20 25 30 Thr Tyr Asn Val Gly Ser Asn

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid

 - (C) STRANDEDNESS single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION:\amidated Tyr
- (xi) SEQUENCE DESCRIPTION: \SEQ ID NO:5:

Lys Cys Asn Thr Ala Thr Cys Ala Thr\Gln Arg Leu Ala Asn Phe Leu Val His Ser Ser Asn Asn Phe Gly Aro Val Leu Pro Pro Thr Asn Val Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:6\
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Asp Asn Thr Ala Thr Lys Ala Thr Gln Arg Leu Ala Asn Phe

1 5 10 15

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

20 25 30

Asn Val Gly Ser Asn Thr Tyr

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- (2) INFORMATION FOR\SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: singlè
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cxs residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

1 5 10 15

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

20 25 30

Asn Val Gly Ser Asn Thr Tyr

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: \37
 - (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

1 5 10 15

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

20 25 30

Asn Val Gly Ser Asn Thr Tyr

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- (2) INFORMATION FOR SEQ IN NO:9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

1 5 10 15

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

20 25 30

Asn Val Gly Ser Asn Thr Tyr

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- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37\amino acids
 - (B) TYPE: amind acid
 - (C) STRANDEDNES\$: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE (peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION; amidated Tyr
- (xi) SEQUENCE DESCRIPTION; SEQ ID NO:10:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

1 5 10 15

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Pro Thr

20 25 30

Asn Val Gly Ser Asn Thr Tyr

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- (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) \triangle OCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val His Ser Ser Ash Asn Phe Gly Pro Ile Leu Pro Ser Thr 25 30 20 Asn Val Gly Ser Asn Thr \Tyr

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe 10 Leu Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr 25 30 Asn Val Gly Ser Asn Thr Tyr

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- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids (B) TYPE: \amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (B) LOCATION: 2,7 (D) OTHER INCORMATION: disulfide bridge between the Cys residues (B) LOCATION: 37(D) OTHER INFORMATION: amidated Tyr (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe 10 Leu Val Arg Ser Ser Asn Asn Pre Gly Pro Ile Leu Pro Ser Thr 20 25 Asn Val Gly Ser Asn Thr Tyr 35 (2) INFORMATION FOR SEQ \ID NO:14: (i) SEQUENCE CHARACTERISTICS (A) LENGTH: 37 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (B) LOCATION: 2,7 (D) OTHER INFORMATION: disulfide bridge between the Cys residues (B) LOCATION: 37
- Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Let Ala Asn Phe
 1 5 10 15

(D) OTHER INFORMATION: amidated Tir

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1/4:

Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr
20 25 30
Asn Val Gly Ser Asn Thr Tyr
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- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARA TERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino adid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linea
- (ii) MOLECULE TYPE: petide
- (ix) FEATURE:
 - (B) LOCATION: 2,7
 - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: amidated Tyr
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

1 5 10 15

Leu Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr

20 25 30

Asn Val Gly Ser Asn Thr Tyr

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